

Sequence Alignment #2

RESULT 4
 AQ480395/c
 LOCUS AQ480395 522 bp DNA linear GSS 23-APR-1999
 DEFINITION RPCI-11-236B22.TV RPCI-11 Homo sapiens genomic clone
 RPCI-11-236B22, genomic survey sequence.
 ACCESSION AQ480395
 VERSION AQ480395.1 GI:4662514
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 522)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
 Venter,J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other_GSSs: RPCI-11-236B22.TJ
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 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.
 FEATURES Location/Qualifiers
 source 1..522
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7590285"
 /db_xref="taxon:9606"
 /clone="RPCI-11-236B22"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 ORIGIN
 Query Match 28.5%; Score 231; DB 15; Length 522;
 Best Local Similarity 98.8%; Pred. No. 2.3e-55;
 Matches 244; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 Qy 1 ACAGGTGTAAGCCACTGCACCCGGGTGATAGCTGGTTTCATTACTCTATTCTTGACCA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 247 ACAGGTGTAAGCCACTGCACCCGGGTGATAGCTGGTTTCATTACTCTATTCTTGACCA 188

Qy	61	CTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAG	120
Db	187	CTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAG	128
Qy	121	CATGTCATGTGCTA---ATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCT	177
Db	127	CATGTCATGTGCTAATTATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCT	68
Qy	178	TTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTATTAGCCCCAGACAT	237
Db	67	TTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTATTAGCCCCAGACAT	8
Qy	238	CACTCCA	244
Db	7	CACTCCA	1